

Automated Machine Learning

Frank Zijun Zhang, PhD

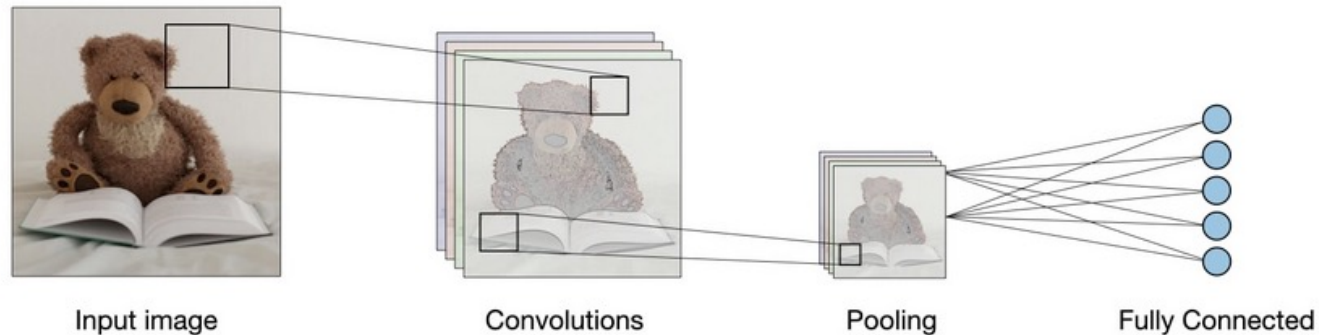
Division of AI in medicine, Cedars-Sinai Medical Center

UCLA QCBio Collaboratory

AutoML workshop, Winter 2023

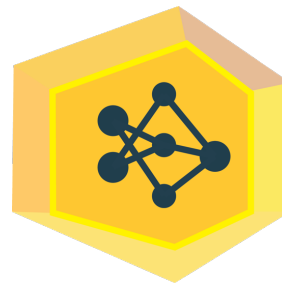
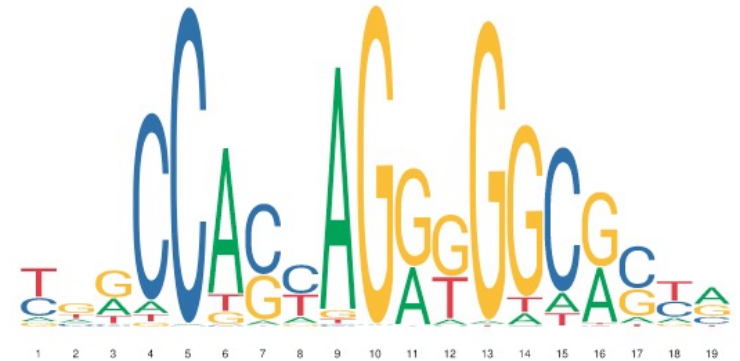
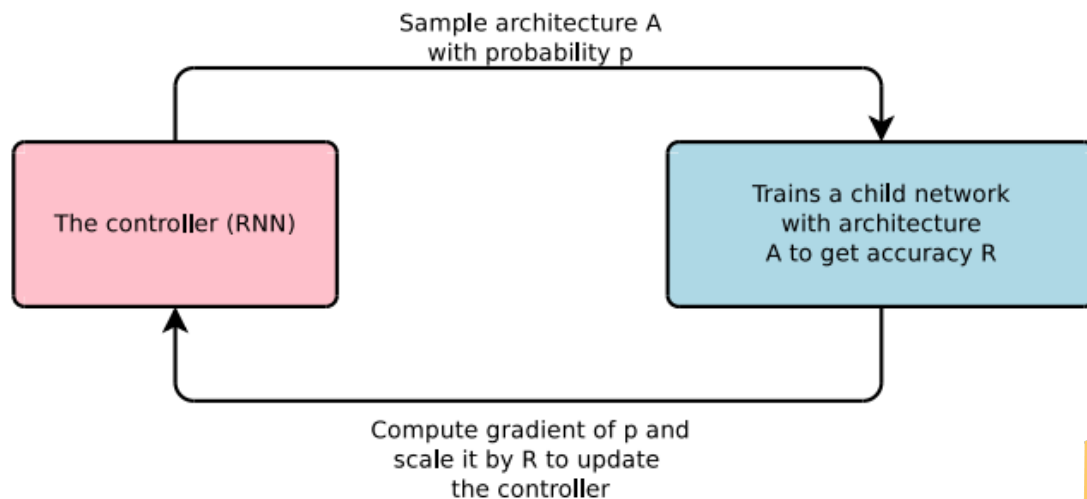
Agenda

- Day1: Build CNNs and Model Evaluation
 - Understand how CNNs model genomic sequences
 - Build CNNs with Tensorflow and PyTorch
 - Model evaluations and tuning




Agenda

- Day2: AutoML and Model Explanation
 - Introduction of reinforcement learning
 - Apply NAS to automate CNN tuning
 - Interpret model and sequence motifs



AMBER

A note on Google Colab and Github

- Go to Github Repo:
- <https://github.com/zhanglab-aim/ucla-automl-workshop>
- Open “UCLA_AutoML_workshop_Day2.ipynb”.
- Click on the Icon  Open in Colab
- Each practice is ~10min; basic code is already implemented in the Notebook
- Explore the Practice questions shown in the slides.

Recap: Building CNNs

- We covered how convolution, pooling, flatten, and fully-connected layers work.
- We implemented a simple CNN model in Keras and PyTorch.
- The model achieved testing AUROC=0.79
 - Can we build a better model?

Day 2: AutoML and Model Explanation

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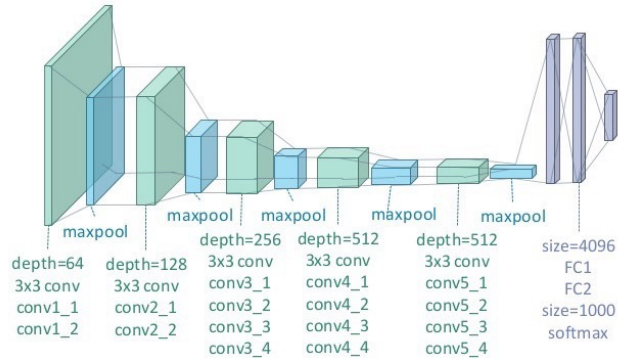
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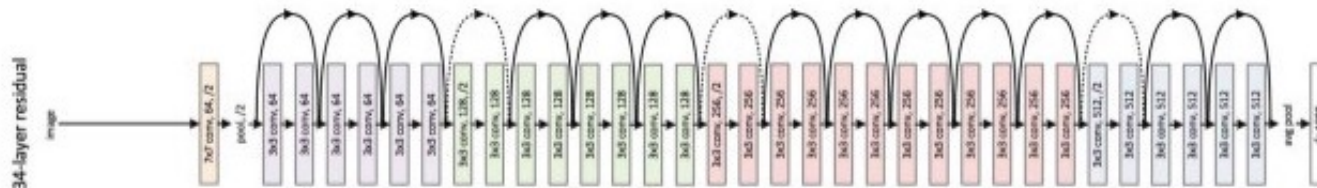
AutoML workshop, Winter 2023

Performance of CNNs is reliant on model architectures

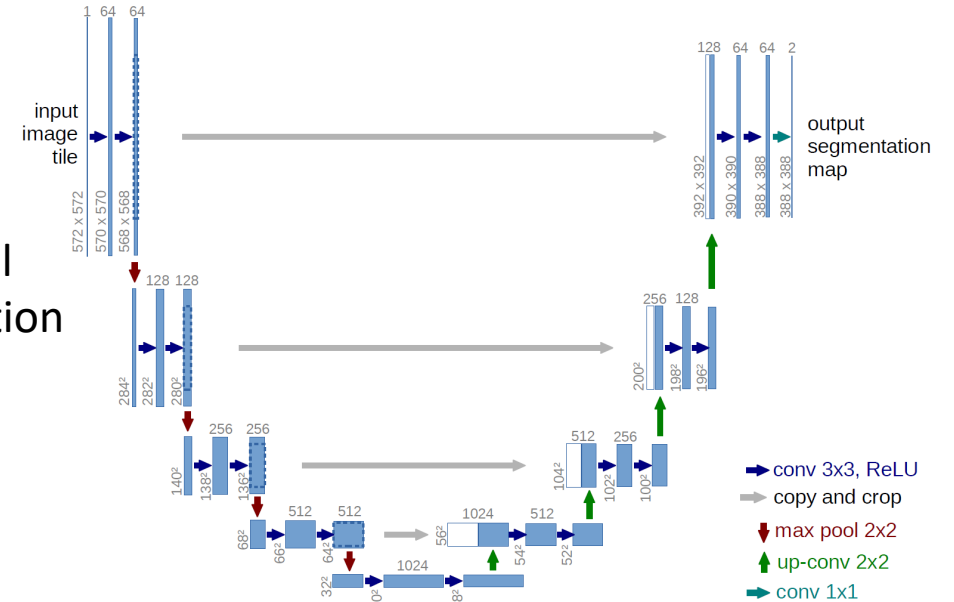
VGG 19



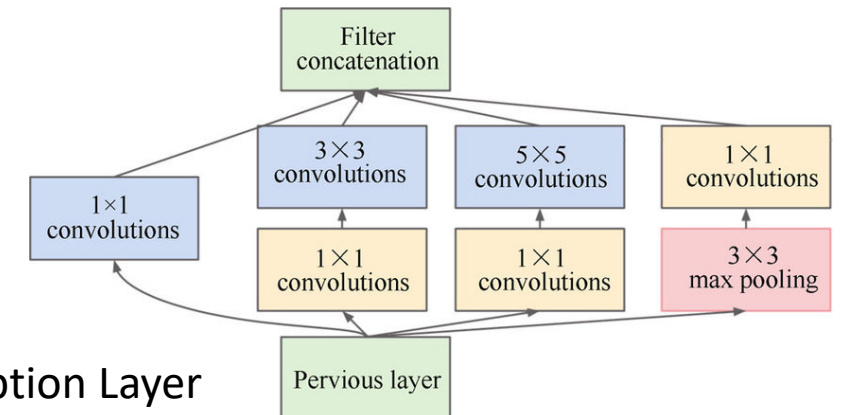
ResNet



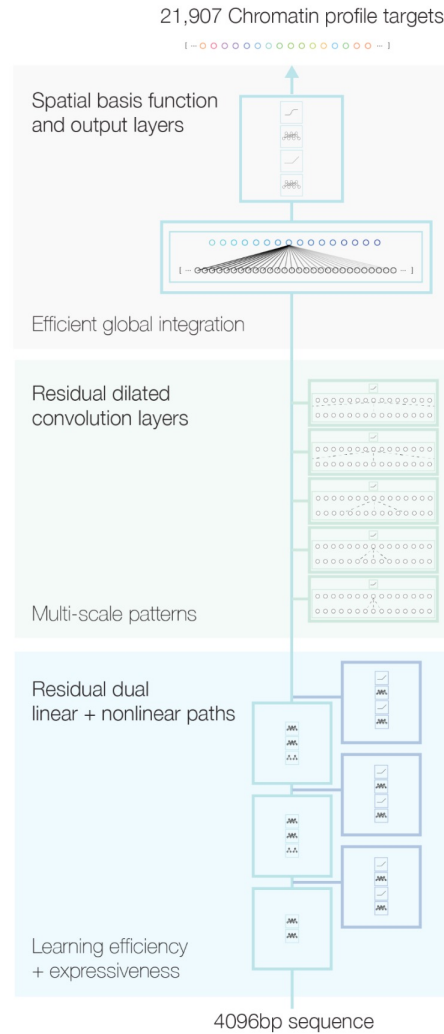
U-Net for medical image segmentation



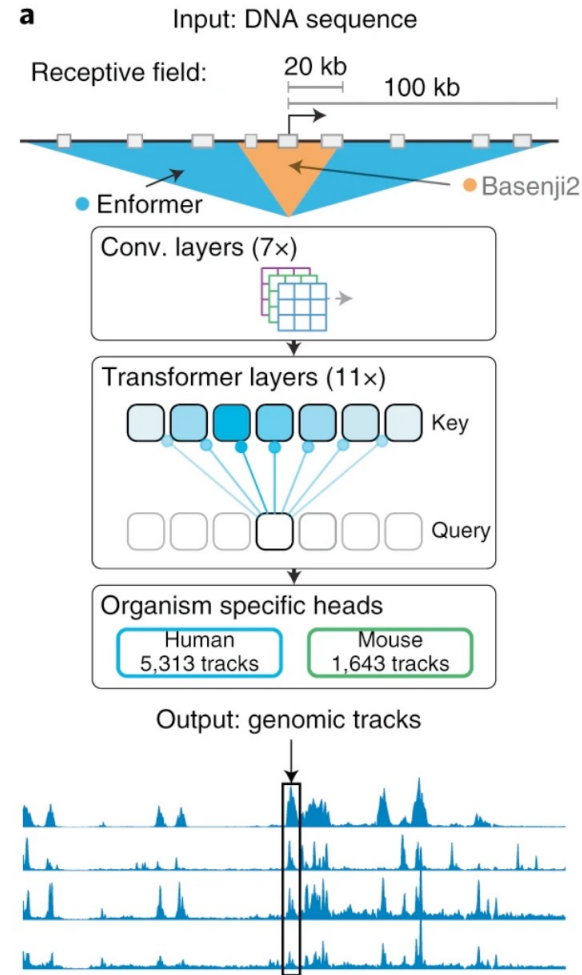
Inception Layer



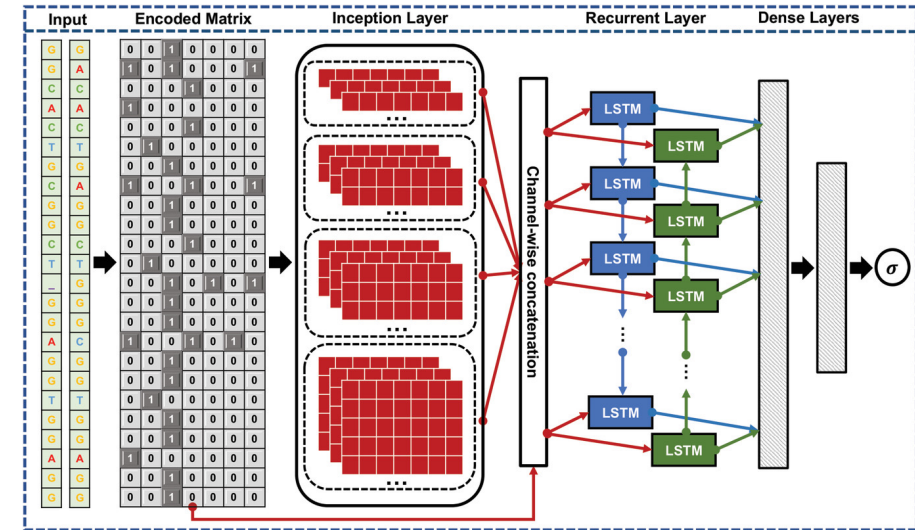
Performance of CNNs is reliant on model architectures



Sei
Chen et al., 2022



Enformer
Avsec et al., 2021



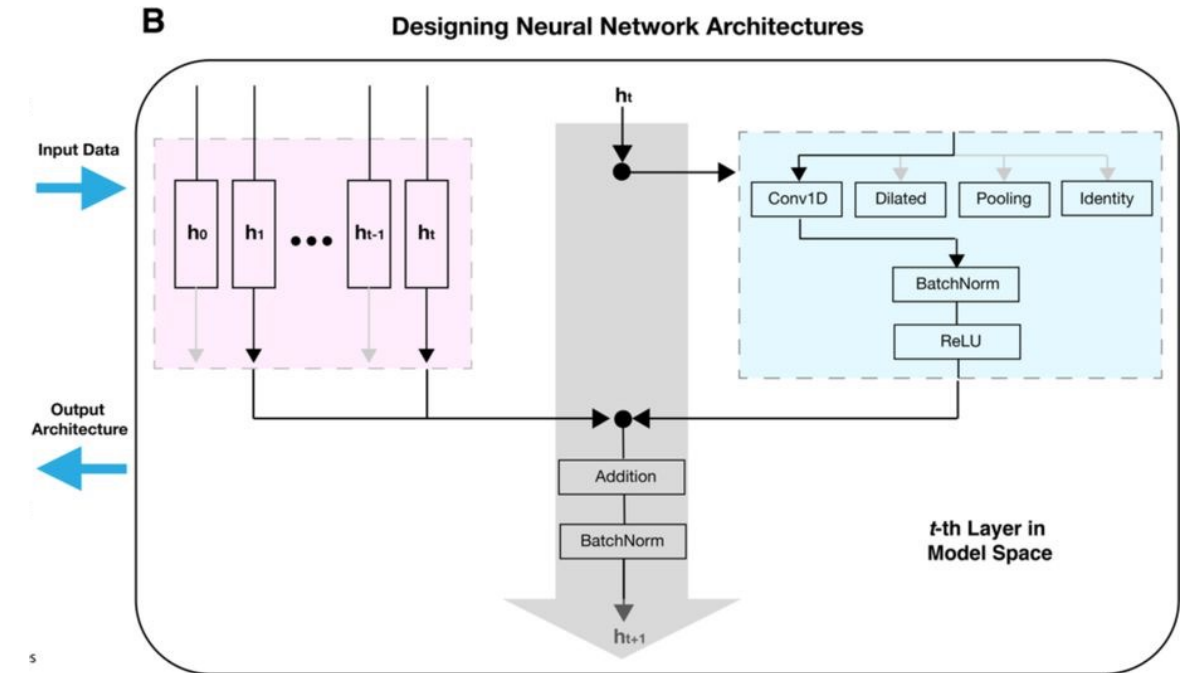
CRISPR-Net
Lin et al., 2020

CNN architecture is important in biomedicine

- A different challenge: Biomedicine and Genomics are data-rich yet highly heterogenous.
 - e.g., single cell RNA-seq vs bulk RNA-seq may require different model complexities.
 - harder to scale-up
- High-stakes prediction: Accurate models are essential for decision-making support and knowledge discovery

What is a CNN's architecture?

- Architecture = Operators + Wiring
 - Conv
 - Pool
 - Flatten
 - FC
- Wiring
 - Skip connections
- For simplicity, we focus on operator searching in this workshop.



Introduction to AMBER

- AMBER is a modularized AutoML framework for genomics and biomedicine, with SOTA search efficiency in 1D tasks.
- `amber.architect` implements AutoML methods
- `amber.modeler` converts a list of Python operators to Models in backend deep-learning libraries (framework-agnostic).

| Model Space | Algorithm | ECG | DeepSEA |
|-------------|-----------|-------------------|------------------|
| WRN | default | 0.57±0.01 | 0.60±0.001 |
| DenseNAS | random | 0.58±0.01 | 0.60±0.001 |
| DenseNAS | original | 0.60±0.01 | 0.60±0.001 |
| WRN | ASHA | 0.57±0.01 | 0.59±0.002 |
| DARTS | GAEA | 0.66±0.01 | 0.64±0.02 |
| AMBER | ENAS | 0.67±0.015 | 0.68±0.01 |

Model Space: a container for layer combinations

- A model space is a List of Lists
- Consider the general order: conv – pool – conv – flatten
- A special operator: *identity* will remove a layer

```
In [8]: from amber import architect
        from amber.backend import Operation
```

```
In [9]: model_space = architect.ModelSpace.from_dict([
        # conv1
        [
            Operation('Conv1d', filters=32, kernel_size=7, activation='relu'), Operation('Conv1d', filters=32, kernel_size=13, activation='re
            Operation('Conv1d', filters=32, kernel_size=7, activation='tanh'), Operation('Conv1d', filters=32, kernel_size=13, activation='ta
        ],
        # pool
        [Operation('Maxpool1d', pool_size=4), Operation('Avgpool1d', pool_size=4), Operation('Identity')],
        # conv2
        [
            Operation('Conv1d', filters=64, kernel_size=7, activation='relu'), Operation('Conv1d', filters=64, kernel_size=13, activation='re
            Operation('Conv1d', filters=64, kernel_size=7, activation='tanh'), Operation('Conv1d', filters=64, kernel_size=13, activation='ta
            Operation('Identity')
        ],
        # flatten
        [Operation('Flatten'), Operation('GlobalAveragePooling1D'), Operation('GlobalMaxPooling1D')],
    ])
    print(model_space)
```

StateSpace with 4 layers and 378 total combinations

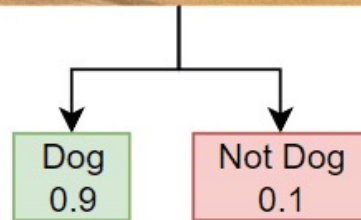
Model Space: a container for layer combinations

- Aside from the moving parts, we need fixed input and output operators.
- A rule of thumb: observe the input feature and output label shapes.
 - For output, find a proper activation function, too.
 - continuous regression: activation='linear'
 - binary/multi-label classification: activation='sigmoid'
 - multi-class classification: activation='softmax'

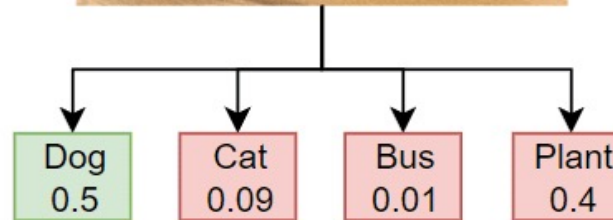
```
input_op = Operation('Input', shape=(200,4))  
output_op = Operation('Dense', units=1, activation='sigmoid')
```

Multi-label vs Multi-class

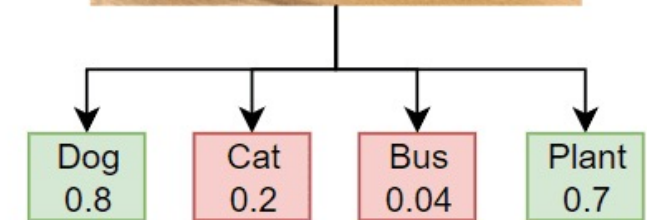
Binary Classification



Multiclass Classification



Multilabel Classification



<https://www.mathworks.com/help/deeplearning/ug/multilabel-image-classification-using-deep-learning.html>

Sampling a CNN from Model Space

- Now we have input/output ops and a viable Model Space, we can sample a list of architecture tokens that translates to a CNN.
- This is implemented as `modeler.sequential.SequentialModelBuilder`
 - input arc= [0, 0, 6, 1]
 - output a CNN model (the model we built in Day 1)

```
model_builder = modeler.sequential.SequentialModelBuilder(  
    inputs_op=input_op,  
    output_op=output_op,  
    model_space=model_space,  
    model_compile_dict=dict(  
        optimizer='adam',  
        loss='binary_crossentropy')  
)
```

```
arc = [0, 0, 6, 1]  
model = model_builder(arc)  
model.summary()
```

Sampling a CNN from Model Space

- More importantly, `SequentialModelBuilder` is framework-agnostic.
- You can switch the backend by `!amber-cli config -b {pytorch, tensorflow_2}` and build CNNs under different frameworks, without changing any code.
- AMBER enables a unified syntax between Tensorflow 1/2 and PyTorch.

Practice 1. Model Space and CNNs

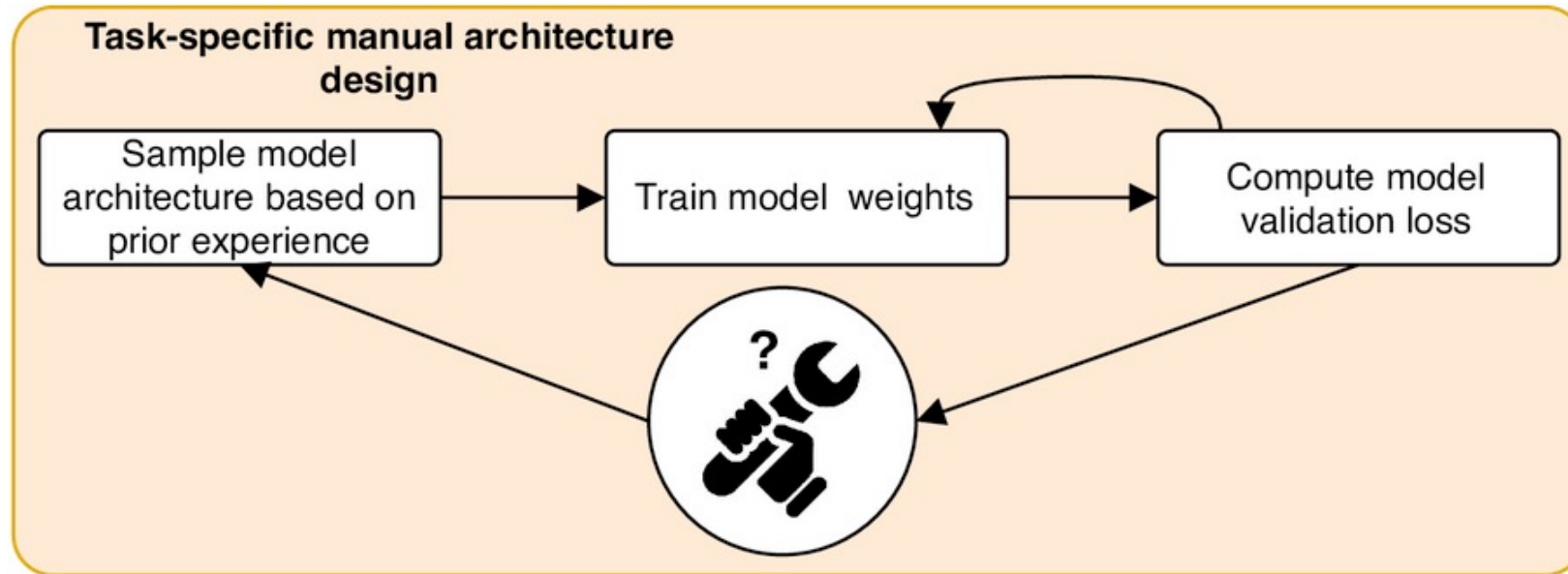
Run Sections 1-2. Define Model Space & Build CNN



- Change the `arc` tokens and/or `model_compile_dict`. Does this increase or decrease your model's performance?
- Change the backend from PyTorch to Tensorflow 2 and re-run Sections 1-2.
- Add another layer of Dense operators in `architect.ModelSpace` after the Flatten layer.
hint: `Operation('Dense', units=16, activation='relu')`
if you change the model space, do you need to change the `arc` tokens when calling `model_builder`?

Manual Tuning of Model Architectures

- As you may have noticed, changing the arc tokens will build different CNNs with varying predictive powers.

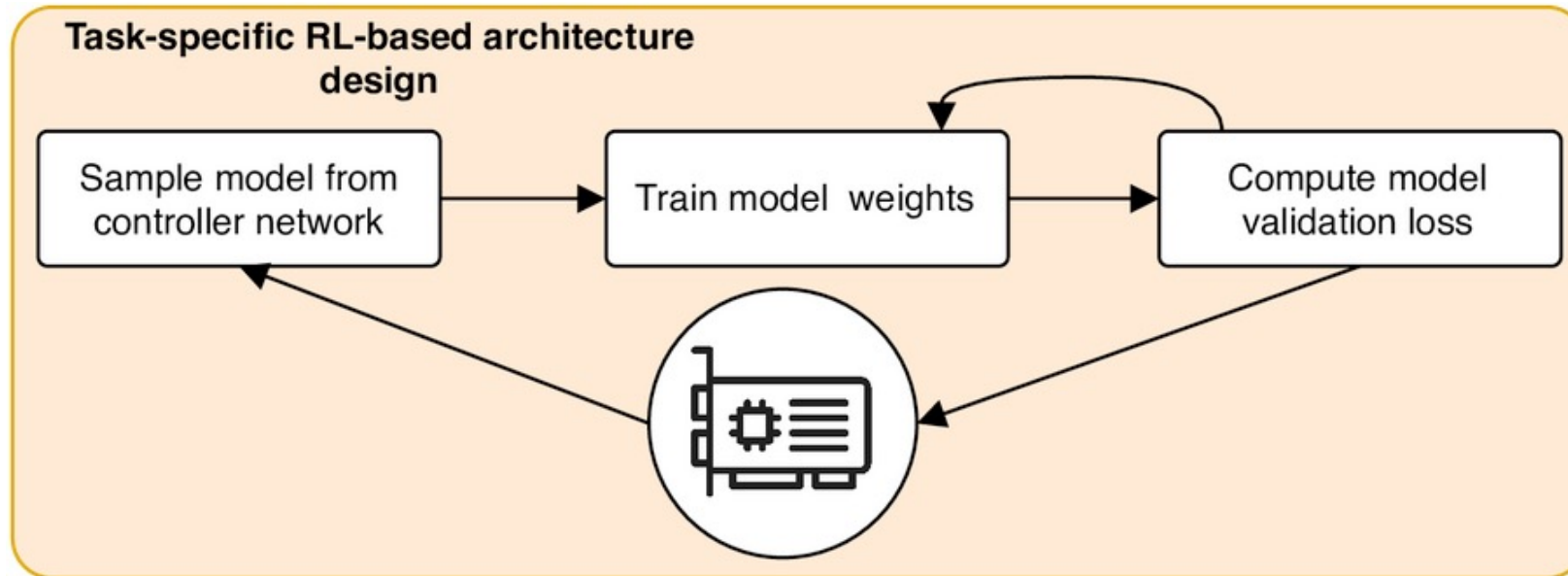


Automated model building process

- At the bare minimum, we can use a for-loop to randomly sample CNNs within a given time budget, and choose the best model.
- However, we can do better by building another model that learns from the history of CNN models to propose arc tokens better than random.

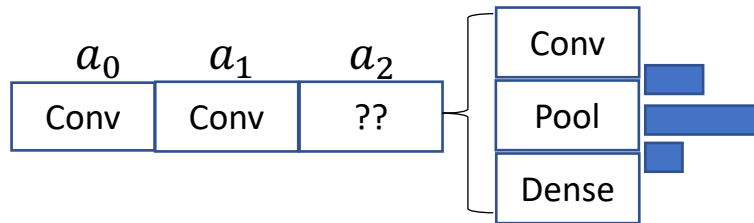
Reinforcement-learning Tuning of Model Architectures

- Reinforcement-learning (RL): reward desired CNN architectures, and penalize underperforming architectures.



Neural Architecture Search with Reinforcement Learning

- A model-based approach: a recurrent neural network (RNN) **controller** model that learns the arc tokens as a sequence.

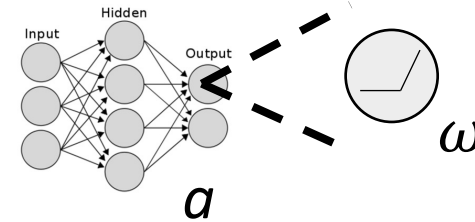


<https://jonathan-hui.medium.com/rl-proximal-policy-optimization-ppo-explained-77f014ec3f12>

Math formulations of controller basics

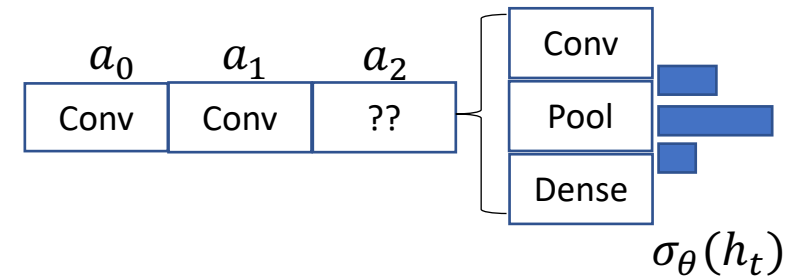
1. To learn a function that maps x to y , optimize its architectures a :

$$y_i = f_{\omega;a}(x_i)$$



2. Sample a_t from the conditional probability $P(a_t|a_{t-1}, \dots, a_0)$ by a Recurrent Neural Network $\sigma_\theta(\cdot)$ with parameters θ :

$$a_t \sim P(a_t|a_{t-1}, \dots, a_0) = \sigma_\theta(h_t)$$



3. Optimize θ w.r.t. to a reward R (usually validation accuracy):

$$\frac{1}{m} \sum_{k=1}^m \nabla_{\theta} \pi(a_k; \theta) (R_k - b)$$

$\pi(a_k; \theta)$: log-likelihood of a_k

R_k : reward for a_k

b : moving average of R



Controller implementation in AMBER

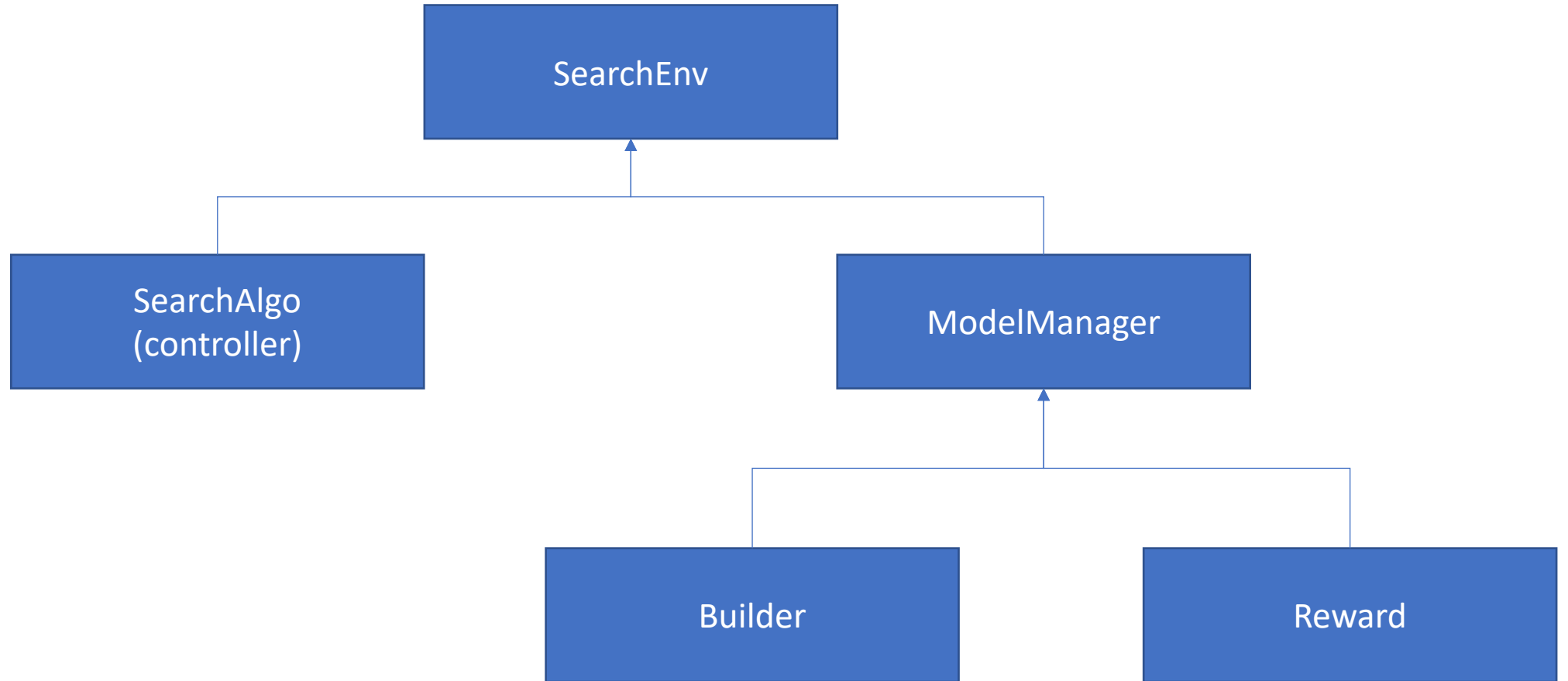
- A controller can be built by parsing a Model Space.
- Initially, the controller is naive and will sample architecture tokens uniformly.
- As we will see, over time these probs are skewed towards better rewards.

```
In [16]: # define a search algorithm  
controller = architect.GeneralController(model_space=model_space)
```

```
In [17]: # action=integers  
# probs=selection probabilities  
controller.get_action()
```

```
Out[17]: (array([4, 1, 0, 2], dtype=int32),  
          [array([[0.16665466, 0.16665043, 0.166673 , 0.1666605 , 0.16669773,  
                  0.16666366]], dtype=float32),  
            array([[0.33329216, 0.33331555, 0.33339226]], dtype=float32),  
            array([[0.14286055, 0.14285785, 0.14282915, 0.14282627, 0.14285736,  
                  0.14287995, 0.14288886]], dtype=float32),  
            array([[0.33334982, 0.33333722, 0.33331293]], dtype=float32)])
```

Components of AMBER NAS



Practice 2. Running AMBER NAS

Run Section 3. Automated Search

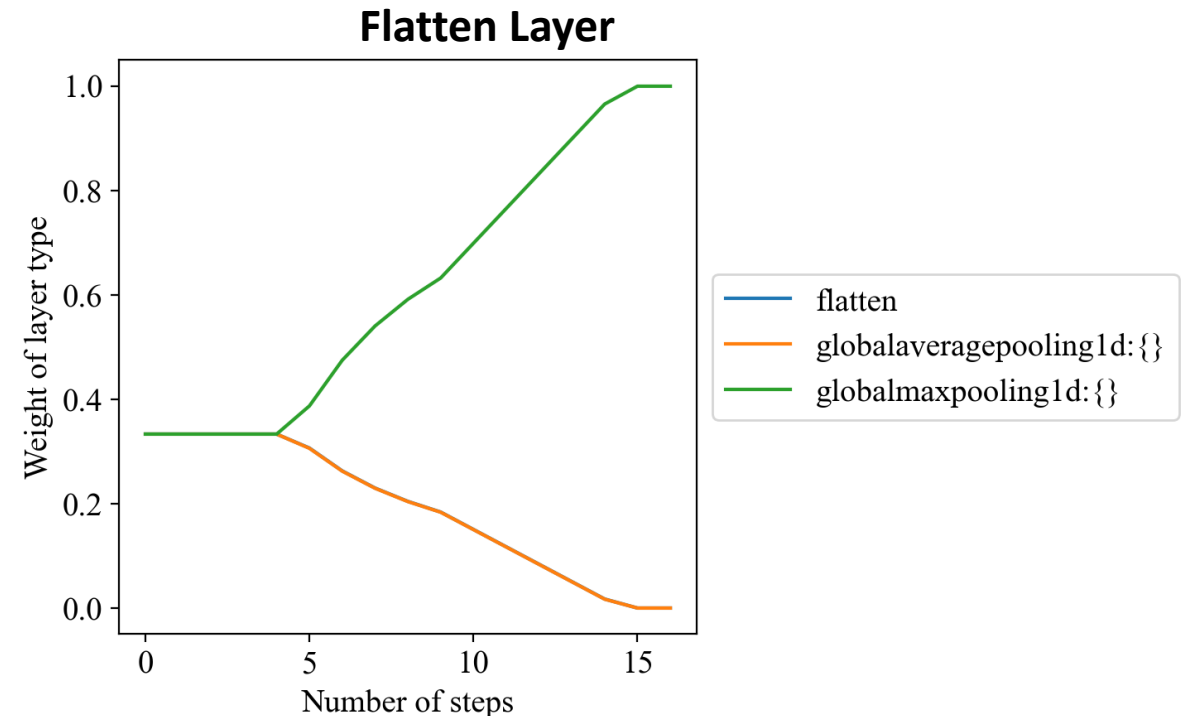
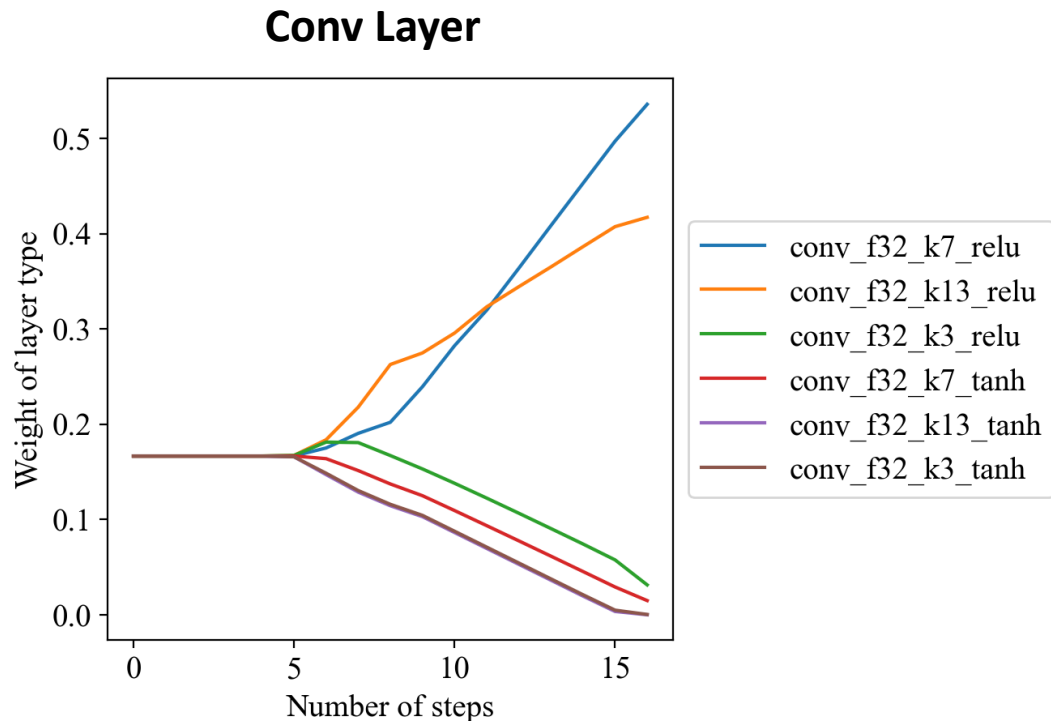
 [Open in Colab](#)

Section 4. Understanding AutoML

- Remember to change your Colab Runtime type to “GPU”.
 - should finish in ~1min.
- Change the backend from PyTorch to Tensorflow_2.
- Change the method of `reward_fn` from “auroc” to a custom callable function to compute Accuracy `acc`; restart the runtime and run all. How does the performance compare?
 - `acc = lambda y_true, y_score: np.mean(y_true==(y_score>0.5).astype(int))`

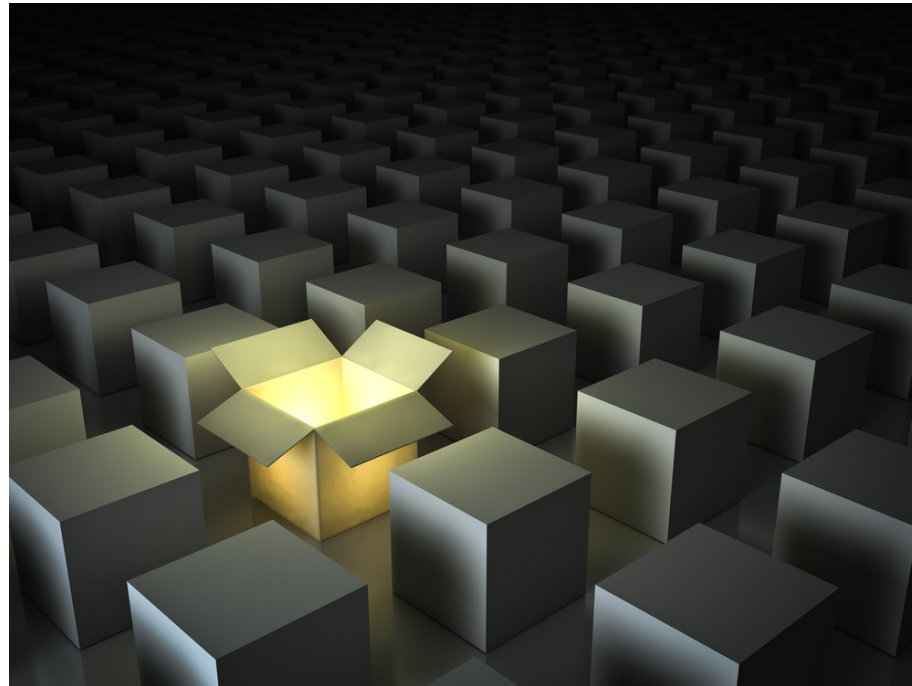
Understanding NAS Principles

- Data-driven model building can reveal insights for our dataset, and for future modeling.
- Sometimes, it can even tell us when a model is too complex for the dataset by selecting *identity* over other operators.



Interpreting the trained model

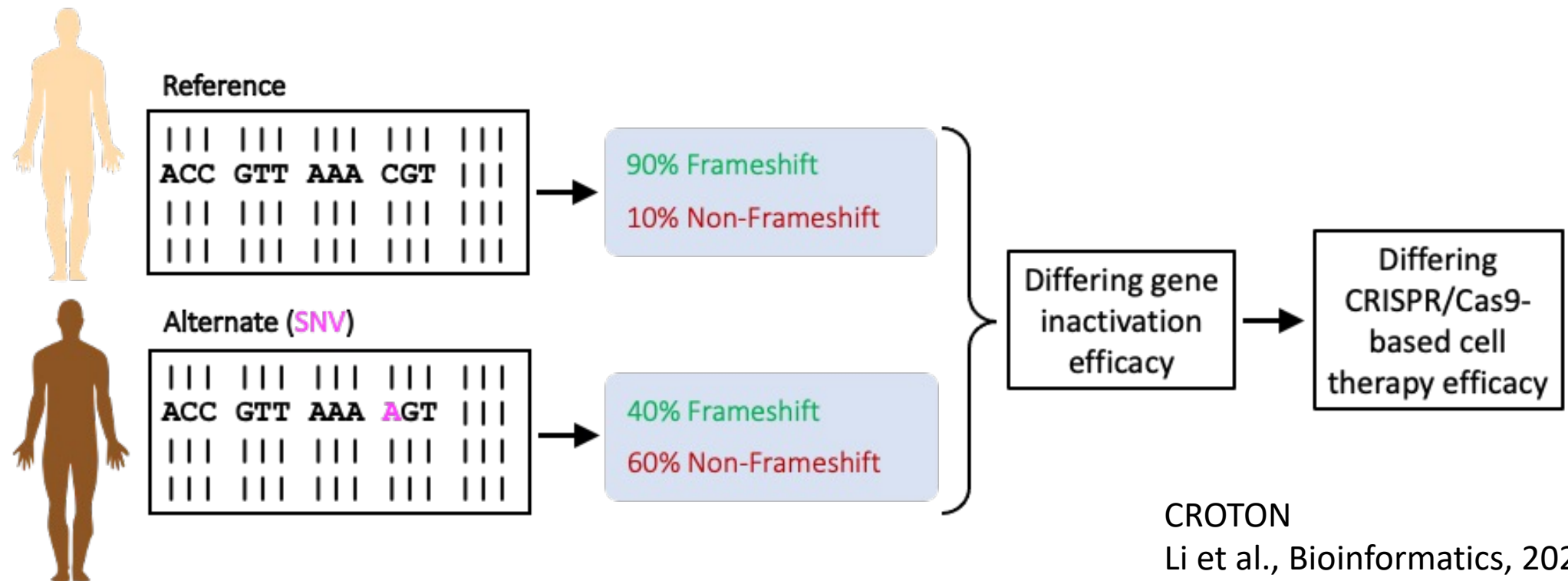
- We can use interpretation methods to understand what evidence is useful for our model.
- For genomic sequences, a popular approach is in-silico mutagenesis (ISM).



(amasterphotographer/Shutterstock)

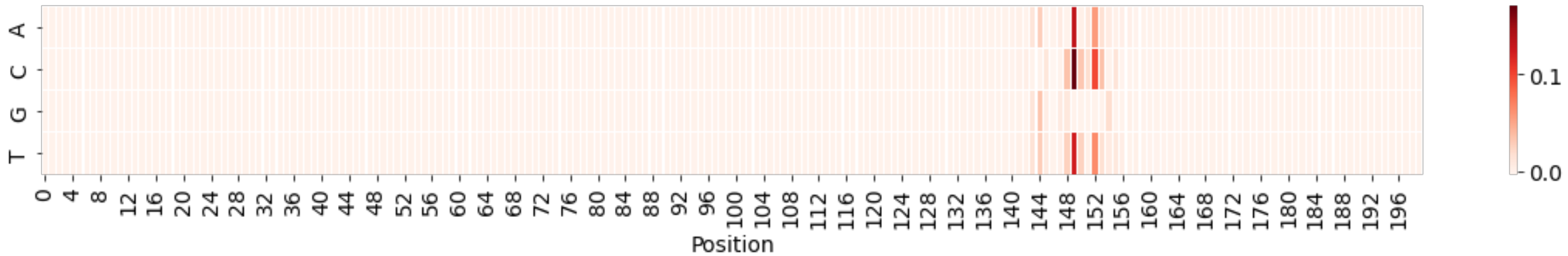
Interpreting the trained model

- in-silico mutagenesis (ISM) introduces mutations to the input sequence, even though such mutations can be rare in natural populations and thus lack of power for analysis.



Saturated ISM

- Saturated ISM exhaustively perturbs every base-pair.
- The resulting score matrix is the same shape as the input sequence.



Practice 3. Model Explanation

Run Section 5.ISM for Model Explanation



- Pick the second-best model and analyze its model explanation results. Is it the same with the best model?
- Compare the focus region with the ground truth motif.
- Think of ways to compute the prediction difference when two letters are changed.

Summary

- Introduction of reinforcement learning
 - Apply NAS to automate CNN tuning
 - Interpret model and sequence motifs
-
- AutoML and its application in Genomics and Biomedicine is an exciting research field.
 - Feel free to reach out to me if you'd like to explore more in this direction.

Q&A

Write your questions in this [Google Doc](#).